FIG.1A

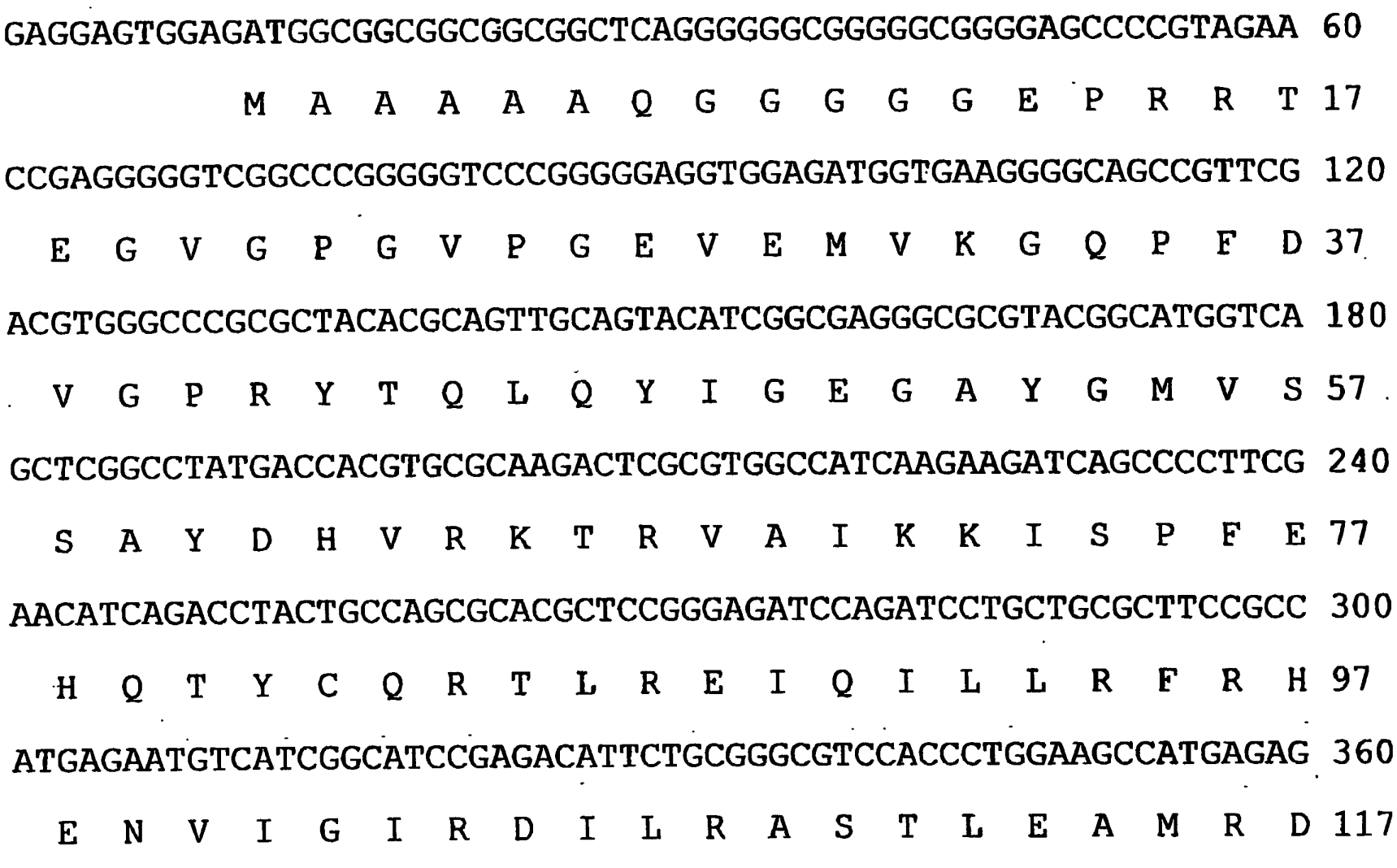

FIG.1B

```
ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420
  V  Y  I  V  Q  D  L  M  E  T  D  L  Y  K  L  L  K  S  Q  Q 137
AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA 480
  L  S  N  D  H  I  C  Y  F  L  Y  Q  I  L  R  G  L  K  Y  I 157
TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA 540
  H  S  A  N  V  L  H  R  D  L  K  P  S  N  L  L  I  N  T  T 177
CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC 600
  C  D  L  K  I  C  D  F  G  L  A  R  I  A  D  P  E  H  D  H 197
ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC 660
  T  G  F  L  T  E  Y  V  A  T  R  W  Y  R  A  P  E  I  M  L 217
TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG 720
  N  S  K  G  Y  T  K  S  I  D  I  W  S  V  G  C  I  L  A  E 237
```

FIG.1C

```
AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA 780
  M  L  S  N  R  P  I  F  P  G  K  H  Y  L  D  Q  L  N  H  I 257
TTCTGGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATAAACGGATCACAG 840
  L  A  L  D  L  L  D  R  M  L  T  F  N  P  N  K  R  I  T  V 277
TGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGGATGAGCCAG 900
  E  E  A  L  A  H  P  Y  L  E  Q  Y  Y  D  P  T  D  E  P  V 297
TGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTAAGGAGCGGCTGA 960
  A  E  E  P  F  T  F  A  M  E  L  D  D  L  P  K  E  R  L  K 317
AGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGGAGGCCCCCTAGC 1020
  E  L  I  F  Q  E  T  A  R  F  Q  P  G  V  L  E  A  P  *    335
```

FIG.1D

CCAGACAGACATCTCTGCACCCTGGGGCCTGGACCTGCCTCCTGCCTGCCCCTCTCCCGC 1080

CAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGGGTG 1140

GAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCAAGG 1200

CCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGTTCA 1260

ATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGTTCT 1320

GGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGGGGC 1380

GCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCTAGT 1440

TTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCGGGC 1500

CGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTGGTG 1560

AGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACCCGT 1620

CTAATATATAAATATAGAGATGTGTCTATGGCTG 1654

FIG.2A

```
GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA 60
          M  A  A  A  A  A  Q  G  G  G  G  G  E  P  R  R  T 17
CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG 120
  E  G  V  G  P  G  V  P  G  E  V  E  M  V  K  G  Q  P  F  D 37
ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA 180
  V  G  P  R  Y  T  Q  L  Q  Y  I  G  E  G  A  Y  G  M  V  S 57
GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG 240
  S  A  Y  D  H  V  R  K  T  R  V  A  I  K  K  I  S  P  F  E 77
AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC 300
  H  Q  T  Y  C  Q  R  T  L  R  E  I  Q  I  L  L  R  F  R  H 97
ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG 360
  E  N  V  I  G  I  R  D  I  L  R  A  S  T  L  E  A  M  R  D 117
```

FIG.2B

```
ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420
  V  Y  I  V  Q  D  L  M  E  T  D  L  Y  K  L  L  K  S  Q  Q 137
AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA 480
  L  S  N  D  H  I  C  Y  F  L  Y  Q  I  L  R  G  L  K  Y  I 157
TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA 540
  H  S  A  N  V  L  H  R  D  L  K  P  S  N  L  L  I  N  T  T 177
CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC 600
  C  D  L  K  I  C  D  F  G  L  A  R  I  A  D  P  E  H  D  H 197
ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC 660
  T  G  F  L  T  E  Y  V  A  T  R  W  Y  R  A  P  E  I  M  L 217
TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG 720
  N  S  K  G  Y  T  K  S  I  D  I  W  S  V  G  C  I  L  A  E 237
```

FIG.2C

```
AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA 780
  M  L  S  N  R  P  I  F  P  G  K  H  Y  L  D  Q  L  N  H  I 257
TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG 840
  L  G  I  L  G  S  P  S  Q  E  D  L  N  C  I  I  N  M  K  A 277
CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC 900
  R  N  Y  L  Q  S  L  P  S  K  T  K  V  A  W  A  K  L  F  P 297
CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA 960
  K  S  D  S  K  A  L  D  L  L  D  R  M  L  T  F  N  P  N  K 317
AACGGATCACAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA 1020
  R  I  T  V  A  E  E  P  F  T  F  A  M  E  L  D  D  L  P  K 337
AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG 1080
  E  R  L  K  E  L  I  F  Q  E  T  A  R  F  Q  P  G  V  L  E 357
```

FIG.2D

```
AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGACCTGCCTCCTGCCTG 1140
  A   P   *                                                    359
CCCCTCTCCCGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCC 1200
CAGGCCGGGGTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCA 1260
GGCAGGCCAAGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGT 1320
GGCCCCAGTTCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTC 1380
TCTGGCAGTTCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGG 1440
AGGGTGGGGGGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAA 1500
CCCCACCCTAGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGA 1560
GCCAGGCCGGGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTT 1620
CTGTGTGTGGTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACC 1680
TCCCTGACCCGTCTAATATATAAATATAGAGATGTGTCTATGGCTG                 1726
```

FIG.3A

```
GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA 60
          M  A  A  A  A  A  Q  G  G  G  G  G  E  P  R  R  T 17
CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG 120
  E  G  V  G  P  G  V  P  G  E  V  E  M  V  K  G  Q  P  F  D 37
ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA 180
  V  G  P  R  Y  T  Q  L  Q  Y  I  G  E  G  A  Y  G  M  V  S 57
GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG 240
  S  A  Y  D  H  V  R  K  T  R  V  A  I  K  K  I  S  P  F  E 77
AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC 300
  H  Q  T  Y  C  Q  R  T  L  R  E  I  Q  I  L  L  R  F  R  H 97
ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG 360
  E  N  V  I  G  I  R  D  I  L  R  A  S  T  L  E  A  M  R  D 117
```

FIG.3B

```
ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420
  V  Y  I  V  Q  D  L  M  E  T  D  L  Y  K  L  L  K  S  Q  Q 137
AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA 480
  L  S  N  D  H  I  C  Y  F  L  Y  Q  I  L  R  G  L  K  Y  I 157
TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA 540
  H  S  A  N  V  L  H  R  D  L  K  P  S  N  L  L  I  N  T  T 177
CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC 600
  C  D  L  K  I  C  D  F  G  L  A  R  I  A  D  P  E  H  D  H 197
ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC 660
  T  G  F  L  T  E  Y  V  A  T  R  W  Y  R  A  P  E  I  M  L 217
TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG 720
  N  S  K  G  Y  T  K  S  I  D  I  W  S  V  G  C  I  L  A  E 237
```

FIG.3C

AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA 780

M L S N R P I F P G K H Y L D Q L N H I 257

TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG 840

L G I L G S P S Q E D L N C I I N M K A 277

CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC 900

R N Y L Q S L P S K T K V A W A K L F P 297

CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA 960

K S D S K A L D L L D R M L T F N P N K 317

AACGGATCACAGTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGA 1020

R I T V E E A L A H P Y L E Q Y Y D P T 337

CGGATGAGCCAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA 1080

D E P V A E E P F T F A M E L D D L P K 357

FIG.3D

```
AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG 1140
  E   R   L   K   E   L   I   F   Q   E   T   A   R   F   Q   P   G   V   L   E 377
AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG 1200
  A   P   *                                                                     379
AGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGACCTGCCTCCTGCCTGCCCCTCTCC 1260
CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG 1320
GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA 1380
AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT 1440
TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT 1500
TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG 1560
GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT 1620
AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG 1680
```

FIG.3E

GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG 1740

GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC 1800

CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1837

FIG.4A

```
GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA 60
          M  A  A  A  A  A  Q  G  G  G  G  G  E  P  R  R  T 17
CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG 120
  E  G  V  G  P  G  V  P  G  E  V  E  M  V  K  G  Q  P  F  D 37
ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA 180
  V  G  P  R  Y  T  Q  L  Q  Y  I  G  E  G  A  Y  G  M  V  S 57
GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG 240
  S  A  Y  D  H  V  R  K  T  R  V  A  I  K  K  I  S  P  F  E 77
AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC 300
  H  Q  T  Y  C  Q  R  T  L  R  E  I  Q  I  L  L  R  F  R  H 97
ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG 360
  E  N  V  I  G  I  R  D  I  L  R  A  S  T  L  E  A  M  R  D 117
```

FIG.4B

```
ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420
  V  Y  I  V  Q  D  L  M  E  T  D  L  Y  K  L  L  K  S  Q  Q 137
AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA 480
  L  S  N  D  H  I  C  Y  F  L  Y  Q  I  L  R  G  L  K  Y  I 157
TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA 540
  H  S  A  N  V  L  H  R  D  L  K  P  S  N  L  L  I  N  T  T 177
CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC 600
  C  D  L  K  I  C  D  F  G  L  A  R  I  A  D  P  E  H  D  H 197
ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC 660
  T  G  F  L  T  E  Y  V  A  T  R  W  Y  R  A  P  E  I  M  L 217
TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG 720
  N  S  K  G  Y  T  K  S  I  D  I  W  S  V  G  C  I  L  A  E 237
```

FIG.4C

```
AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA 780
 M  L  S  N  R  P  I  F  P  G  K  H  Y  L  D  Q  L  N  H  I 257

TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG 840
  L  G  I  L  G  S  P  S  Q  E  D  L  N  C  I  I  N  M  K  A 277

CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC 900
  R  N  Y  L  Q  S  L  P  S  K  T  K  V  A  W  A  K  L  F  P 297

CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA 960
  K  S  D  S  K  A  L  D  L  L  D  R  M  L  T  F  N  P  N  K 317

AACGGATCACAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA 1020
  R  I  T  V  A  E  E  P  F  T  F  A  M  E  L  D  D  L  P  K 337
```

FIG.4D

```
AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG 1080
  E   R   L   K   E   L   I   F   Q   E   T   A   R   F   Q   P   G   V   L   E 357
AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG 1140
  A   P   *                                                                     359
```

FIG.4E

AGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGACCTGCCTCCTGCCTGCCCCTCTCC 1200

CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG 1260

GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA 1320

AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT 1380

TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT 1440

TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG 1500

GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT 1560

AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG 1620

GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG 1680

GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC 1740

CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1777

FIG.5A

```
          1                                                          60
SMAPK3V1  GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA
SMAPK3V2  GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA
SMAPK3    GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA
SMAPK3V3  GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA
SMAPK3V4  GAGGAGTGGAGATGGCGGCGGCGGCGGCTCAGGGGGGCGGGGGCGGGGAGCCCCGTAGAA

          61                                                         120
SMAPK3V1  CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG
SMAPK3V2  CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG
SMAPK3    CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG
SMAPK3V3  CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG
SMAPK3V4  CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG
```

FIG.5B

```
          121                                                       180
SMAPK3V1  ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA
SMAPK3V2  ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA
SMAPK3    ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA
SMAPK3V3  ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA
SMAPK3V4  ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA

          181                                                       240
SMAPK3V1  GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG
SMAPK3V2  GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG
SMAPK3    GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG
SMAPK3V3  GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG
SMAPK3V4  GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG
```

FIG.5C

```
          241                                                       300
SMAPK3V1  AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC
SMAPK3V2  AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC
SMAPK3    AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC
SMAPK3V3  AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC
SMAPK3V4  AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC

          301                                                       360
SMAPK3V1  ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
SMAPK3V2  ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
SMAPK3    ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
SMAPK3V3  ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
SMAPK3V4  ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
```

FIG.5D

```
          361                                                      420
SMAPK3V1  ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC
SMAPK3V2  ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC
SMAPK3    ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC
SMAPK3V3  ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC
SMAPK3V4  ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC

          421                                                      480
SMAPK3V1  AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA
SMAPK3V2  AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA
SMAPK3    AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA
SMAPK3V3  AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA
SMAPK3V4  AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA
```

FIG.5E

```
          481                                                      540
SMAPK3V1  TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA
SMAPK3V2  TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA
SMAPK3    TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA
SMAPK3V3  TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA
SMAPK3V4  TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA

          541                                                      600
SMAPK3V1  CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC
SMAPK3V2  CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC
SMAPK3    CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC
SMAPK3V3  CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC
SMAPK3V4  CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC
```

FIG.5F

601 660

SMAPK3V1 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC

SMAPK3V2 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC

SMAPK3 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC

SMAPK3V3 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC

SMAPK3V4 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC

661 720

SMAPK3V1 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG

SMAPK3V2 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG

SMAPK3 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG

SMAPK3V3 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG

SMAPK3V4 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG

FIG.5G

```
          721                                                       780
SMAPK3V1  AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA
SMAPK3V2  AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA
SMAPK3    AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA
SMAPK3V3  AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA
SMAPK3V4  AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA

          781                                                       840
SMAPK3V1  TTCTGG----------------------------------------------------
SMAPK3V2  TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG
SMAPK3    TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG
SMAPK3V3  TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG
SMAPK3V4  TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG
```

FIG.5H

```
          841                                                       900
SMAPK3V1  ----------------------------------------------------------
SMAPK3V2  CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC
SMAPK3    CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC
SMAPK3V3  CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC
SMAPK3V4  CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC

          901                                                       960
SMAPK3V1  ------------------CCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA
SMAPK3V2  CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA
SMAPK3    CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA
SMAPK3V3  CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA
SMAPK3V4  CCAAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATA
```

FIG.5I

```
          961                                                        1020
SMAPK3V1  AACGGATCACAGTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGA
SMAPK3V2  AACGGATCACAGTGG-------------------------------------------
SMAPK3    AACGGATCACAGTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGA
SMAPK3V3  AACGGATCACAGTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGA
SMAPK3V4  AACGGATCACAGTGG-------------------------------------------

          1021                                                       1080
SMAPK3V1  CGGATGAGCCAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA
SMAPK3V2  ---------------CCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA
SMAPK3    CGGATGAGCCAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA
SMAPK3V3  CGGATGAGCCAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA
SMAPK3V4  ---------------CCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCTA
```

FIG.5J

```
          1081                                                    1140
SMAPK3V1  AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG
SMAPK3V2  AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG
SMAPK3    AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG
SMAPK3V3  AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG
SMAPK3V4  AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG

          1141                                                    1200
SMAPK3V1  AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGA--------------
SMAPK3V2  AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGA--------------
SMAPK3    AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGA--------------
SMAPK3V3  AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG
SMAPK3V4  AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG
```

FIG.5K

```
          1201                                                        1260
SMAPK3V1  ------------------------------------CCTGCCTCCTGCCTGCCCCTCTCC
SMAPK3V2  ------------------------------------CCTGCCTCCTGCCTGCCCCTCTCC
SMAPK3    ------------------------------------CCTGCCTCCTGCCTGCCCCTCTCC
SMAPK3V3  AGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGACCTGCCTCCTGCCTGCCCCTCTCC
SMAPK3V4  AGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGACCTGCCTCCTGCCTGCCCCTCTCC

          1261                                                        1320
SMAPK3V1  CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
SMAPK3V2  CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
SMAPK3    CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
SMAPK3V3  CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
SMAPK3V4  CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
```

FIG.5L

1321 1380

SMAPK3V1 GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA

SMAPK3V2 GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA

SMAPK3 GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA

SMAPK3V3 GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA

SMAPK3V4 GTGGAGCATGGGCCTGGCCACCTCTCTCCTTTGCTGAGGCCTCCAGCTTCAGGCAGGCCA

1381 1440

SMAPK3V1 AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT

SMAPK3V2 AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT

SMAPK3 AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT

SMAPK3V3 AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT

SMAPK3V4 AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT

FIG.5M

```
          1441                                                    1500
SMAPK3V1  TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT
SMAPK3V2  TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT
SMAPK3    TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT
SMAPK3V3  TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT
SMAPK3V4  TCAATCTCCCGCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT

          1501                                                    1560
SMAPK3V1  TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG
SMAPK3V2  TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG
SMAPK3    TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG
SMAPK3V3  TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG
SMAPK3V4  TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGGTGGGG
```

FIG.5N

```
          1561                                                    1620
SMAPK3V1  GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT
SMAPK3V2  GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT
SMAPK3    GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT
SMAPK3V3  GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT
SMAPK3V4  GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCCT

          1621                                                    1680
SMAPK3V1  AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG
SMAPK3V2  AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG
SMAPK3    AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG
SMAPK3V3  AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG
SMAPK3V4  AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG
```

FIG.5O

```
          1681                                                    1740
SMAPK3V1  GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG
SMAPK3V2  GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG
SMAPK3    GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG
SMAPK3V3  GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG
SMAPK3V4  GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTG

          1741                                                    1800
SMAPK3V1  GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC
SMAPK3V2  GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC
SMAPK3    GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC
SMAPK3V3  GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC
SMAPK3V4  GTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC
```

FIG.5P

1801

SMAPK3V1	CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG	1654
SMAPK3V2	CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG	1726
SMAPK3	CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG	1786
SMAPK3V3	CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG	1837
SMAPK3V4	CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG	1777

FIG.6A

```
          1                                                          60
SMAPK3V1  MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
SMAPK3V2  MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
SMAPK3    MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
SMAPK3V3  MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
SMAPK3V4  MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY

          61                                                         120
SMAPK3V1  DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
SMAPK3V2  DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
SMAPK3    DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
SMAPK3V3  DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
SMAPK3V4  DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
```

FIG.6B

```
          121                                                        180
SMAPK3V1  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
SMAPK3V2  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
SMAPK3    VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
SMAPK3V3  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
SMAPK3V4  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL

          181                                                        240
SMAPK3V1  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
SMAPK3V2  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
SMAPK3    KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
SMAPK3V3  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
SMAPK3V4  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
```

FIG.6C

```
          241                                                        300
SMAPK3V1  NRPIFPGKHYLDQLNHIL----------------------------------------
SMAPK3V2  NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
SMAPK3    NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
SMAPK3V3  NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
SMAPK3V4  NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD

          301                                                        360
SMAPK3V1  --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
SMAPK3V2  SKALDLLDRMLTFNPNKRITV----------------AEEPFTFAMELDDLPKERL
SMAPK3    SKALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
SMAPK3V3  SKALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
SMAPK3V4  SKALDLLDRMLTFNPNKRITV----------------AEEPFTFAMELDDLPKERL
```

FIG.6D

```
          361
SMAPK3V1  KELIFQETARFQPGVLEAP---------- ----------    335
SMAPK3V2  KELIFQETARFQPGVLEAP---------- ----------    359
SMAPK3    KELIFQETARFQPGVLEAP---------- ----------    379
SMAPK3V3  KELIFQETARFQPGVLEAP---------- ----------    379
SMAPK3V4  KELIFQETARFQPGVLEAP---------- ----------    359
```